

**Amendments to the Claims:**

This listing of claims will replace all prior versions, and listings, of claims in the application:

**Listing of Claims:**

1-31. (Canceled)

32. (Currently amended) A method for inhibiting the expression of a target gene through ~~an intracellular RNA interference~~ a post-transcriptional gene silencing mechanism in a cell or organism that expresses the targeted gene, comprising the steps of:

a) providing a composition comprising an mRNA-cDNA hybrid duplex prior to contacting said cell or said organism, wherein the mRNA-cDNA hybrid duplex is ~~capable of~~ used by the cell or organism as a template to generate small gene-silencing effectors inhibiting the expression of said targeted gene in said cell or organism, wherein said expression is inhibited through said ~~intracellular RNA interference~~ post-transcriptional gene silencing mechanism; and

b) contacting said cell or said organism with said composition under conditions such that the expression of said gene in said cell or said organism is inhibited,

wherein the mRNA is a ribonucleic acid sequence in the sense orientation of said targeted gene and the cDNA is a deoxyribonucleic acid sequence in the anti-sense orientation of said targeted gene, and wherein the mRNA-cDNA hybrid duplex forms between said mRNA and said cDNA in a complementary region containing more than 500 base pairs.

33. (Canceled)

34. (Previously presented) The method of Claim 32, wherein said cell or said organism expresses said targeted gene *in vivo*, wherein said cell or said organism is a cell, tissue, or organ selected from the group consisting of cancerous cells, liver, and skin.

35. (Currently amended) The method of Claim 32, wherein said targeted gene comprises a ~~gene selected from the group consisting of sonic hedgehog (Shh),~~ beta-catenin, ~~and~~ bel-2 gene.

36. (Currently amended) The method of Claim 32, wherein said mRNA-cDNA hybrid duplex inhibits the expression of said targeted gene, wherein said targeted gene comprises ~~a region selected from the sonic hedgehog sequence amplified by SEQ ID NOs: 12, 13, 14, and 15,~~ a  $\beta$ -catenin sequence encoding its amino acid domain from position 306 to 644, ~~and a bel-2 sequence amplified by SEQ ID NOs: 8 and 9.~~

37. (Canceled)

38. (Previously presented) The method of Claim 32, wherein said cell is a prokaryotic cell.

39. (Canceled)

40. (Previously presented) The method of Claim 38, wherein said cell is a bacterial cell.

41. (Previously presented) The method of Claim 32, wherein said cell or said organism is a cell or organism of an eukaryote.

42. (Original) The method of Claim 41, wherein said eukaryote is a vertebrate.

43. (Original) The method of Claim 41, wherein said eukaryote is a mouse.

44. (Original) The method of Claim 41, wherein said eukaryote is chimpanzee.

45. (Original) The method of Claim 41, wherein said eukaryote is a human being.

46-54. (Canceled)

55. (Previously presented) The method of Claim 32, wherein the composition consists of an mRNA-cDNA hybrid duplex capable of inhibiting the expression of said targeted gene, wherein the mRNA is a ribonucleic acid sequence in the sense orientation of said targeted gene and the cDNA is a deoxyribonucleic acid sequence in the anti-sense orientation of said targeted gene, wherein the mRNA-cDNA hybrid duplex forms between said mRNA and said cDNA in a complementary region containing more than 500 base pairs.

56-57. (Canceled)

58. (Previously presented) The method of Claim 55, wherein said targeted gene is expressed in a cell or organism *in vivo*, wherein said cell or said organism is a cell, tissue, or organ selected from the group consisting of cancerous cells, liver, and skin.

59. (Currently amended) The method of Claim 55, wherein said targeted gene comprises a ~~gene selected from the group consisting of sonic hedgehog (Shh), beta-catenin, and bel-2 gene.~~

60. (Currently amended) The method of Claim 55, wherein said mRNA-cDNA hybrid duplex inhibits the expression of said targeted gene, wherein said targeted gene comprises ~~a region selected from the sonic hedgehog sequence amplified by SEQ ID NOs: 12, 13, 14, and 15, a  $\beta$ -catenin sequence encoding its amino acid domain from position 306 to 644, and a bel-2 sequence amplified by SEQ ID NOs: 8 and 9.~~

61. (Previously presented) The method of Claim 55, wherein said cell is a prokaryotic cell.

62. (Canceled)

63. (Previously presented) The method of Claim 61, wherein said cell is a bacterial cell.

64. (Previously presented) The method of Claim 55, wherein said cell or said organism is a cell or organism of an eukaryote.

65. (Previously presented) The method of Claim 64, wherein said eukaryote is a vertebrate.

66. (Previously presented) The method of Claim 64, wherein said eukaryote is a mouse.

67. (Previously presented) The method of Claim 64, wherein said eukaryote is chimpanzee.

68. (Previously presented) The method of Claim 64, wherein said eukaryote is a human being.

69. (Currently amended) A method for inhibiting the expression of a target gene through ~~an intracellular RNA interference~~ a post-transcriptional gene silencing mechanism in a cell or organism that expresses the targeted gene, comprising the steps of:

a) providing a composition comprising an mRNA-cDNA hybrid duplex prior to contacting said cell or said organism, wherein the mRNA-cDNA hybrid duplex is ~~capable of used by the cell or organism as a template to generate small gene-silencing effectors~~ inhibiting the expression of said targeted gene in said cell or said organism, wherein said expression is inhibited through said intracellular RNA interference post-transcriptional gene silencing mechanism; and

b) contacting said cell with said composition under conditions such that the expression of said gene in said cell is inhibited,

wherein the mRNA is a ribonucleic acid sequence in the sense orientation of said targeted gene and the cDNA is a deoxyribonucleic acid sequence in the anti-sense orientation of said targeted gene, and wherein the mRNA is a full-length transcript of said targeted gene larger than 500 base pairs.

70. (Previously presented) The method of Claim 69, wherein the mRNA is an unspliced mRNA transcript of the targeted gene.

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71. (Previously presented) The method of Claim 69, wherein the mRNA is a spliced mRNA transcript of the targeted gene.